array and] being capable of taking part in hybridization reactions.

8. (Amended) A method of analyzing a polynucleotide [sequence], by the use of a support to the surface of which is attached an array of oligonucleotides comprising the whole or a [chosen] defined part of a complete set of oligonucleotides of chosen lengths, [the different oligonucleotides occupying separate cells of the array], which method comprises labelling the polynucleotide [sequence] or fragments thereof to form labelled material, applying the labelled material under [hybridisation] hybridization conditions to the array, and observing the location of the label on the surface associated with particular members of the set of oligonucleotides.

9. (Amended) [A] The method according to claim 8, applied to the study of differences between [polynucleotide sequences] polynucleotides, wherein the array of oligonucleotides comprises the whole or a [chosen] defined part of the complete set of oligonucleotides of chosen lengths corresponding to the polynucleotide sequences.

Claim 19, line 9, change "nucleotidfe" to --nucleotide--.

Please add new claim 24 as follows:

--24. Apparatus for analyzing a polynucleotide, the apparatus comprising a support segregated into at least two cells, each cell having attached thereto defined oligonucleotides, where the sequence of the oligonucleotides of a first cell is different than the sequence of the oligonucleotides of a second cell.--

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REMARKS

Favorable reconsideration is respectfully requested.

The claims are 1-24.

The indication that claim 17-20, 22 and 23 are allowable is acknowledged with appreciation. However, for reasons discussed below, it will now be explained why all the claims in the case are allowable.

The above amendment is responsive to points set forth in the Official Action.

New claim 24, which is similar to claim 18 but does not include the "covalent" terminology, is presented by the above amendment.

Claims 1-16 and 21 have been rejected under 35 U.S.C. 112, as being indefinite in several respects.

With regard to claim 1, line 3, (as well as the remaining claims) the term "a chosen part" has been changed to "a defined part" to clarify what is intended.

With regard to the rejected term "sequences" in claim 2, line 6, such no longer appears.

The Official Action has questioned what are the metes and bounds of the term "pairs" in claim 3, line 2. In reply, any two oligonucleotides can constitute a pair. Usually but not necessarily, the two nucleotides will have something in common, e.g. they will be the same length or have several individual nucleotides in common. In this regard, if the Examiner prefers, applicants are agreeable to deleting the term "pairs of" in claim 3, line 2.

Claim 21 is said to be indefinite. In this regard, the Official Action states:

> It is unclear whether applicant means to claim a square shaped cell wherein the claim limitation directed to 10-100 microns is one side of said square. Alternatively, does applicant mean any irregularly shaped cell where 10-100 microns is the maximum linear dimension? Does applicant wish to claim a circular cell shape where 10-100 microns is the diameter of said cell? Clarification is requested.

In reply, in claim 21, the dimensions relate to any one dimension of the pixels. Similar language is used to describe, for example, very small pore sizes in laboratory filters. Like small filter pores, the pixel shape can vary slightly from circular to square, any one dimension ranging in size from the claimed dimensions. Since the specification describes the cells as pixels, there is ample support for this point and for maintaining main 21 in its present form.

Turning to the rejections of prior art, claims 1-3, 6, and 8-10 have been rejected under 35 U.S.C. 102(b) as being clearly anticipated by Brigati et al.

Further, claims 1-4, and 8-11 have been rejected under 35 U.S.C. 102(b) as being clearly anticipated by Saiki et al.

These rejections are respectfully traversed.

The Brigati et al. and Seiki et al. references describe attaching polynucleotides to be analyzed onto a support and then probing the support with a defined oligonucleotide in order to study or analyze something unknown with respect to the attached polynucleotide.

The presently claimed array, on the other hand, involves a novel "reverse" dot blot technique in which "defined" oligonucleotides are attached to the support and the unknown polynucleotides are studied or analyzed by providing conditions for annealing the polynucleotides to the attached defined oligonucleotides.

This contrasts with the traditional dot blot techniques and solid support described in Brigati et al. and Seiki et al. because these references teach solid supports having attached polynucleotides which are in no way "defined". At the most, the DNA attached to the supports described in these references, may or may not contain a certain gene or gene mutation.

For the foregoing reasons, it is apparent that the rejections on prior art are untenable and should be withdrawn.

No further issues remaining, allowance of this